Figure 1A

IgG1 library

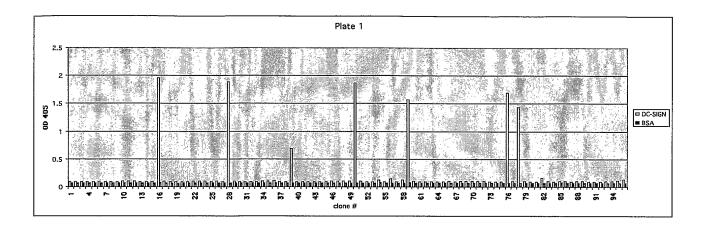


Figure 1B

IgG2a library

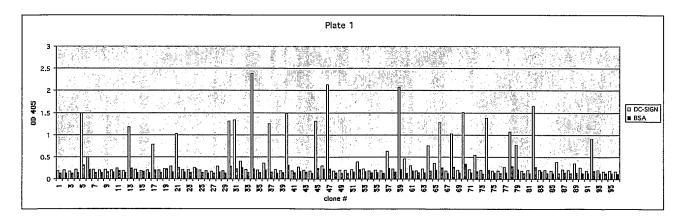


Figure 2

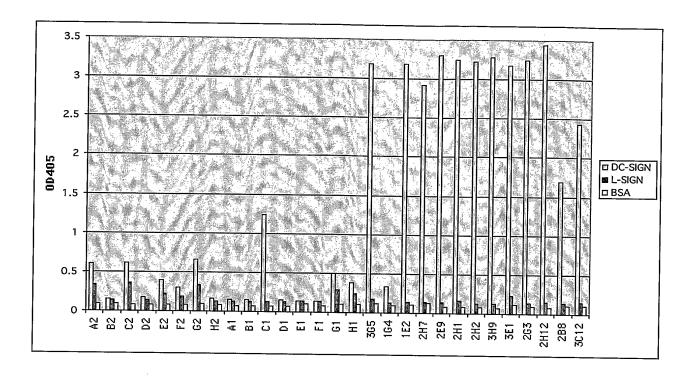
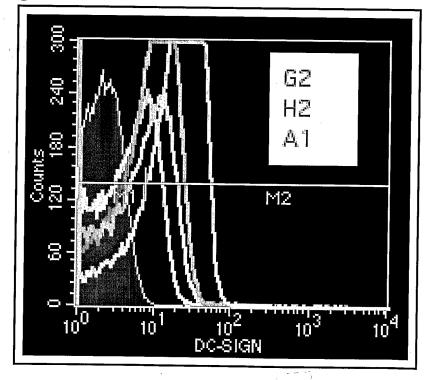


Figure 3



A1= clone 1 H2=clone 15 G2=clone 16 WO 2005/058244 PCT/US2004/041788 3/7

Figure 4a

Light chain sequences

Major		7																																			Q			P -+-		
										10)									20)									30)									40		
1 1 1 1 1	D D D D D	IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Q Q P Q Q Q Q Q	M M M M M M	T T T T T T	00000000	S T T T T T	P T T T T T	Assssss	ល ល ល ល ល ល ល	L L Q L L Q L L	ន	A A A A A A	ម្ម មេខ មេខ មេខ	V L L L L	00000000	EDDDDDDD	T R R R R R R R	V V V V V V	T T T T T T	I I I I	T T S T T S S	00000000	R R R R R R R R R	A T A A A A	ច្ច ច្ច ច្ច ច្ច	EQQHQQQH	N D D D D D D D	IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	H N N S N R N	и и о и и о	Y Y Y Y Y N	L L L L L L	A N N N N N N	W W W W W	Y Y Y Y Y Y	0000000 00000	99999999	N K K K K K K	Q P P P P P P	1 2 2 3 3	G4LC B8LC CH1LC CH2LC GC12LC GE1LC GE7LC GH9LC
Major	_	y																																			N					
																				•										•										-+- 80		
41 41 41 41 41 41 41	GDDDDDD	K G G G G G G	S T T T T T T	P V V V V V V	Q K K K K K K	L L L L	L L L L L	V I I I I I I	Y Y Y Y Y Y	N Y Y Y Y Y Y	A T T T T T	K S S S S S S S	T R R S R R S S	LLLLLLL	A H H Q H H P Q	V S S S S S S S	00000000	V V V V V V	9999999	000000000000000000000000000000000000000	R R R R R R R R	F F F F F F F F	SSSRSSR	99999999	S S S Y S S S Y	G G G G G R G	ល	99999999	T T T T T	Q D D D D D D	F Y Y Y Y Y	00 00 00 00 00 00	L L L	K T T T T T	IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	N S S S S S S	S N N N N N	T T T	Q A E A A E	P Q Q Q Q	1 2 2 2 3 3 3	G4LC 2B8LC 2H1LC 2H2LC 3C12LC 3E1LC 3E7LC 3H9LC
Major	it	V							_																								_									
																					00		-							_												
81 81 81 81 81 81	EEEEEE	000000	F L F I L	G A V A A A A	N T T T T	Y Y Y Y Y	Y F F F F F	0000000	9999999	HQQQQQQ	FGGGGGG	W D K D K D		TLLLLLL	P P P P P P	W F W Y F W P	T T T T T	3 3 3 4 4 4 5 7	9999999	RSGGSGG	9999999	T T T T T	K T K T K K	TILLI	EEEEE	I I I I	K K K K K K	R R R R R R R	A A A A A		(SE (SE (SE (SE (SE		III III III	1 0 1 0 1 0 1 0 1 0	10 10 10 10 10		10) 12) 13) 14) 15)))))				LG4LC 2B8LC 2H1LC 2H2LC 3C12LC 3E1LC 3E7LC 3H9LC

Figure 4 b

EVQLQQSGPE	LVKPGASVK	KISCKASGYSF	T - G Y Y M H W V K Q	Majority						
10 20 30 40										
E V Q L Q Q S G P G E V Q L Q Q S G P E E V Q L Q Q S G P E E V Q L Q Q S G P E E V Q L Q Q S G P E E V Q L Q Q S G P E	L V K P S Q S L S L V K P G A S V K L V K P G T S V K L V K P G T S V K L V K P G T S V K L V K P G A S V K	S L A C S V T G Y S I K I S C K A S G Y S F K I S C K A S G Y S F K I S C K A S G Y S F K I S C K A S G Y S F K I S C K A S G Y S F K I S C K A S G Y S F K I S C K A S G Y S F	T S G Y Y W N W I R C T T - G Y Y M H W V K C T T - G Y Y M H W V K C T T - G Y Y I H W V R C T T - G Y Y I H W V R C T T - G Y Y I H W V R C T T - G Y Y M H W V K C T T - G Y Y M H W V K C T T - G Y Y M H W V K C	19 1G4HC 1 1H2HC 2 2B8HC 2 2H1HC 2 2H2HC 2 3C12HC 2 3E1HC						
SHVKSLEWIG	RINPYNGAT	T S Y N Q N F K D K A	A S L T V D K S S T T V	Majority						
50	30									
S P G N K L E W M G S H V K S L E W I G S H V K S L E W I G R H V K S L E W I G R H V K S L E W I G S H V K S L E W I G S H V K S L E W I G S H V K S L E W I G	Y I S Y D - G N S R I N P Y N G A T R I N P Y S G A T R I N P Y S G A T R I N P Y S G A T R I N P Y N G A T R I N P Y N G A T R I N P Y N G A T R I N P Y N G A P R I N P Y N G A P	S D Y N P S F K N R I T S Y N Q N F K D K A T Y Y N H N F K D K A T S Y N Q S F K D K A T S Y N Q S F K D K A T S Y N Q N F K D K A T S Y N Q N F K D K A P S Y N Q N F K D K A F S Y N Q N F K D K A F S Y N Q N F K D K A	I S I T R D T S K N Q I A S L T V D K S S T T \ A T L T V H K S S T T \ A S L T V D K S S T T I A S L T V D K S S T T I A S L T V D K S S T T I A S L T V D E S S T T I A S L T V D E S S T T I A S I T A D T S S N T I	F 1G4HC 7 1H2HC 7 2B8HC A 2H1HC A 2H2HC 7 3C12HC F 3E1HC A 3E7HC						
YMEVHSLTSE	DSAVYYCVR	R S N D G Y Y S Y P M	M D Y W G Q G T S V T V	V Majority +-						
96	90 100 110 1									
F L R L N S L T T E ID NO: 18) Y M E V H S L T S E Y M E V H S L T S E Y M E V H S L T S E Y M E V H S L T S E Y M E V H S L T S E Y M E V H S L T S E	D T A T Y Y C V R D S A V Y Y C V R D S A V Y Y C V R D S A V Y Y C V R D S A V Y Y C V R D S A V Y Y C V R D S A V Y Y C V R	R D D S G R F P Q R S N D G Y Y S Y P M R S N D G Y Y S Y P M R S N D G Y Y S Y P M R S N D G Y Y S Y P M R S N D G Y Y S Y P M R S N D G Y Y S Y P M R S N D G Y Y S Y P M	Q W G Q G T L V T V S A M D Y W G Q G S S V A V M D Y W G Q G T S V T V M D Y W G Q G T S V T V M D Y W G Q G T S V T V M D Y W G Q G T S V T V M D Y W G Q G T S V T V M D Y W G Q G T S V T V V D Y W G Q G T S V T V	A 1G4HC (SEQ V 1H2HC V 2B8HC V 2H1HC V 2H2HC V 3C12HC V 3E1HC						
S S (SEQ ID NO: 19	9)			Majority						
S S (SEQ ID NO: 2 S S (SEQ ID NO: 2 S S (SEQ ID NO: 2 S S (SEQ ID NO: 3	21) 2B8HC 22) 2H1HC 23) 2H2HC 24) 3C12HC 25) 3E1HC									

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5 4

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Figure 4c

IgG2a library Heavy Chains

WGQGTLVTVSAAKTT WGQGTSVTVSSAKTT WGQGTSVTVSSAKTT WGQGTSVTVSSAKT WGQGTLVTVSAAKTT WGQGTSVTVSSAKT SVQLQQSGAELVKPGASVKLSCTASGENIK *DTYMH* WVKQRPEQGLEWIG R*IDPANGNTKYDPKFQG* KATITADISSNTAYLQLSSLISEDTAVYYCARD *YYGIYVDY* WGQGTTLIVSSAK EVQLQQSGAELARPGASVKLSCKASGYTFR SYMMQ WVKQRPGQGLEWIG AIYPGDGDTRYTQKFKG KATITADKSSSTAYMQLSSLASEDSAVYFCARG GLKSFYAMDHMGQGTSVTVSSAK WGQGTSVTVS SVQLQQSGPDLVKPGASVRISCKTSGFTFA NYIH WVKQRPGQGLEWIG WIFPGNFKTEYNEKFKG KATLTADKSSSTAYMQLSSLFSEDSAVYFCARG YGYAVDY SVQLQQSGPDLVKPGASVRISCKTSGFTFA SYYIH WVKQRPGQGLEWIG WIFPGNFKTEYNEKFKG KATLITADRSSSTAYMQLSSLTSEDSAVYFCARG YGYAVDY EVQLQQSGTELVRPGALVKLSCKASGFNIK DYFMH WVKQRPEQGLEWIG WIDPKNGNTIYDPKFQV KASITADISSNTAYLQLISLISEDTAVYYCTTT YPNALDY SVQLQQSGPDLVKPGASVRISCKASGFTFA SYYIH WVKQRPGQGLEWIG WIFPGNNNTKSNEKFKG KATLTADKSSSTAYMQLSSLTSEDSAVYFCARG YGYAVDY EVQLQQSGPDLVKPGASVRISCKASGFTFA SYYIH WVKQRPGQGLEWIG WI*FPGNNNTKSNEKFKG* KATLTADKSSSTAYMQLSSLTSEDSAVYFCARG YGXAVDY RISISKDNSESQVELKMDSLQTDDTAKYYCARI NFGILGY EVQLQQSGAELVKPGASVKLSCTASDENIK *DTYIQ* WVKQRPEQGLEWVG *RIDPANGEIKYDPKFQG* KATITADTSSNTAYLQLSSLTSEDTAVYVCTAY *FLVY* SVQLKESGPGLVAPSQSLSITCTVSGFSLS RYTVH WIRQPPGKGLEWLG MIWGGGTTDYNSALKS .5 (SEQ ID NO: 35) (SEQ ID NO: 31) (SEQ ID NO: 30)

Light chains

WYQQKPDGTVKLLIY YTSRLHS GVPSRFSGSGSGTDYSLTISNLEQEDIATYFC QQGNTLPPT FGGGTKLEIKR 11 (SEQ ID G Π DVVMIÇIPLILISVIIGQPASISC KSSQSLLDSDGKIYLN WILMRPGQSPKRLIY LVSKLDS GVPDRFIGSGSGTDFTLKISRVEAEDLGVYFC WQDIHFPHV HVRCWDQAGIT 2(SEQ ID VS WYQQKPDQSPKLLIY GSSNRST GVPDRFTGSGSATDFTLTISSVQAEDLADYHC GQSYNYPPT FGGGTKLEIKR 3(SEQ ID П H WYQQKPDGTVKLLIY YTSRLHS GVPSRESGSGSGTDYSLTISNLEQADIATYFC QQGKTLPWT FGGGTKLEIKR 7(SEQ ID П DIVOTOSPASLAVSLGORATISC KASOSVDYDGDSYMN WYQOKPGQPPKILIY AASNIHS GVPSRFSGSGSGTDYSLTISNLEQADIATYFC *QQGKTLPWT* FGGTKLEIKR 15(SEQ NO: 44) VA WYQQKPGQSPKLLIY SASYRYT GVPDRFTGSGSGTDFTFTISSVQAEDLAVYYC *QQHYITPLT F*GAGTKLELKR 1(SEQ VA WYQQKPGQSPKLLIY WASTRHT GVPDRFTGSGSGTDYTLTISSVQAEDLALYYC QQYYSTPRT FGGGTKLEIKR 4 (SEQ WYQQKPDGTVKLLLY YTSTLHS GVPSRESGSGSTDYSLTISNLEPEDVATYYC QQYGNLPYT FGGGTKLEIKR 5(SEQ WYQQNPGQSIKILIY WASTRHI GVPDRFIGSGSGIDYILIINSVQAEDLILYYC QQHYITPLI FGAGTKLELKR 8(SEQ RYQMTQTISSLSASLGDRVIISC SASQDIINYIN DIQCTQTTSSLSASLGDRVTISC RASQDISNYLN RYPDAQTISSLSASLGDRVIISC RASQDISNYLN RHOMTOSHKFMSTSVGDRVSITC KASQDVSTAVA DIAMTQSHKFMSTPVGDRVSITC KASQDVSTA SIVLTQSPKSMSMSVGERVTLSC KASENVGTY DIVLTQSHKFMSTSVGDRVSITC KASQDVSTA NO: 41) NO: 37)

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Figure 5A IgG1 library

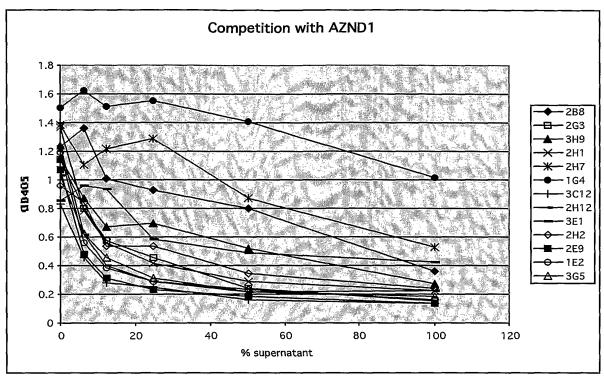


Figure 5B IgG2a library

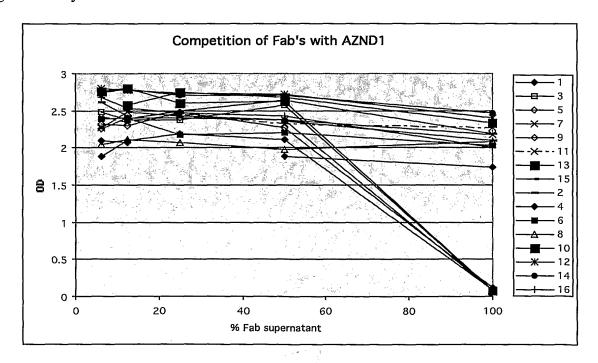


Figure 6

